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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1484.97 Seconds  
(without alignments)  
12007.805 Million cell updates/sec

Title: US-09-807-933B-4

Perfect score: 1101

Sequence: 1 atgaagttacttactattac.....caggtgttcaagaataa 1101

## Scoring table:

IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

EST:  
1: em\_estsba:\*  
2: em\_estsba:\*  
3: em\_estsba:\*  
4: em\_estsba:\*  
5: em\_estsba:\*  
6: em\_estsba:\*  
7: em\_estsba:\*  
8: em\_estsba:\*  
9: em\_estsba:\*  
10: em\_estsba:\*  
11: em\_estsba:\*  
12: em\_estsba:\*  
13: em\_estsba:\*  
14: em\_estsba:\*  
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16: em\_estsba:\*  
17: em\_estsba:\*  
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24: em\_estsba:\*  
25: em\_estsba:\*  
26: em\_estsba:\*  
27: em\_estsba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164.6	15.0	691	10	BE585661 EST#6PSP6
2	127.6	11.6	450	13	BI200729 O105F8.r
3	119	10.8	444	13	BI190695 13g10f8.r
4	113.2	10.3	426	13	BI187295 alh11f8.r
5	75	6.8	215	13	BI190568 12e11f8.r
6	58.2	5.3	289	13	BI191461 k3g10f8.r

Result No.	Score	Query Match	Length	DB ID	Description
7	58.2	5.3	299	13	BI187393
8	57	5.2	274	13	BI186678 d3c10f8.r
9	57	5.2	280	13	BI190362
10	57	5.2	289	13	BI189728
11	49.2	4.5	559	9	AU013377
12	46.8	4.3	541	14	BQ767726 EBR008_SQ
13	45.6	4.1	243	10	AW285303
14	44	4.0	539	9	AU013529
15	44	4.0	558	10	AW564379
16	43.8	4.0	406	10	BE355499
17	43.8	4.0	500	10	AW565843
18	43	3.9	989	17	CNS02HA4
19	42.8	3.9	806	17	CNS04AE2
20	42.2	3.8	805	17	CNS04RM2
21	41.6	3.8	381	10	BE428196
22	41.2	3.7	478	13	BU378871
23	41.2	3.7	490	13	BU355220
24	41.2	3.7	684	14	C25558
25	41.2	3.7	716	13	AU060245
26	41.2	3.7	716	13	BU389338
27	41.2	3.7	748	17	AZ183618
28	40.8	3.7	450	17	FR0025683
29	40.6	3.7	547	17	AZ181216
30	40.6	3.7	605	10	AW565746
31	40.6	3.7	619	17	FR0006944
32	40.4	3.7	280	13	BU373726
33	40.4	3.7	481	13	BU379386
34	40.4	3.7	773	17	CNS01VVG
35	40.4	3.7	824	17	AZ185454
36	40.2	3.7	470	13	BU383671
37	40.2	3.7	540	13	BU379507
38	40	3.6	550	17	FR0043207
39	39.8	3.6	451	17	AZ498168
40	39.8	3.6	476	13	BU384477
41	39.8	3.6	482	13	BU382550
42	39.8	3.6	491	13	BU385517
43	39.8	3.6	933	17	AZ204694
44	39.8	3.6	979	17	CNS06PDW
45	39.6	3.6	459	13	BU348931

## ALIGNMENTS

RESULT 1  
BE585661  
LOCUS  
DEFINITION  
CDNA library Triticum aestivum cDNA clone EST#6PSP6\_D02\_d2\_014, mRNA sequence.  
ACCESSION  
BE585661  
VERSION  
BE585661.1  
KEYWORDS  
GI:9838604  
ORGANISM  
Triticum aestivum  
broad wheat.  
REFERENCE  
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S. The structure and function of the expressed portion of the wheat genome - Kansas State University. Fusarium graminearum infected spike cDNA library unpublished (2000)  
JOURNAL  
COMMENT  
US Department of Agriculture, Agriculture Research Service, Plant Science and Entomology Unit  
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State University, Manhattan, KS 66506, USA  
Tel: 785-532-2367  
Fax: 785-532-6167  
Email: jpf@alfalfa.ksu.edu  
Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20  
Seq primer: SP6.  
Location/Qualifiers

FEATURES  
source  
1. 691  
/organism="Triticum aestivum"  
/cultivar="Suma13"  
/db\_xref="taxon:4565"  
/clone="EST#68P6.D02.d2.014"  
/clone\_lib="KSU wheat Fusarium graminearum infected spike  
cDNA library"

/issue\_type="spike"  
/dev\_stage="Adult Plant"  
/lab\_host="E. coli JM109"  
/note="Vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;  
plants were grown in the greenhouse. Spikes were sprayed  
with Fusarium graminearum (at what stage). Total RNA, and  
poly(A) RNA were prepared from infected spikes. cDNA was  
prepared using the SmartTM PCR cDNA synthesis kit from  
Clontech. cDNA was cloned into the pGEM-T easy vector  
from Promega."

BASE COUNT 135 a 196 c 163 g 197 t  
ORIGIN

Query Match 15.0%; Score 164.6; DB 10; Length 691;  
Best Local Similarity 62.0%; Pred. No. 1.3e-37;  
Matches 282; Conservative 0; Mismatches 164; Indels 9; Gaps 1;

464 GTGGGCGCTCTGTGAAGCGTGTCACTACTGCTTATTTGGATTCTGTAAAGGCTCTCTGA 523  
160 GTGCTGCTTCTGGAAGTGTCACTCTGATCTGTGAGACTGTGCAAGCTTCTTGTCT 219  
524 GCTGGCCCGGTAAAGCCCAATGTCAATCTCTGTCAAGTCTGTAAAGATGTGTCA 583  
220 CTGGAGGCGCAAGCCCAAGTCAAGCCCTCTGTGCTTGAAGTGTGACAAAAAGACACC 279  
584 CTGCCCTTAGTACAGCAATGTCCAAAGTGTGTAAAGTGTGTAAAGTGTATGTGA 643  
280 CCATCACTTAAGTCAAGCCGCTCAAGGTTGTGAAGTGTGTGCTTGTGCTTGA 339  
644 ACACAAACAGCGCTTGGGCTGTAAAGATATCTTGCCTATGTTGGCTGCTGCCA 703  
340 CTAACTACTCCCTTGGGCTGTCAAGCAAGACCTTGTAGGTTACGCTTCAAGC 399  
704 TCAGTGTGTGTGAATCTGCTGTGCTGTTTCTTGTGAACCTTCACTTCA 763  
400 TTGCTGTGTGTGACAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 459  
764 CCTGTGTGTGTGAAGATGTGTATTCAGATCACTTAACCTGTGTGTGTGTGTGTGT 823  
460 GTCCCGTAAAGGAAAGATATGTTCAGTCCACCAACCTGTGTGTGTGTGTGTGTGT 517  
824 CTTCTACTGTGTCTTGAATGTCAATGCGCGTGTGTGTGTGTGTGTGTGTGTGTGT 883  
518 -----TGATTAACCACTTGAATGTATGATGCGCGGTGTGTGTGTGTGTGTGTGT 570  
884 GTTGTCTCAAGCAATGT 918  
Db 571 GATGACCTCTGAGTTGTGGCAAGCCCTGTGTGTGT 605

RESULT 2  
BI200729 450 bp mRNA linear EST 10-JUL-2001  
LOCUS o105f5.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
DEFINITION library Fusarium sporotrichioides cDNA clone o105f5 5', mRNA  
sequence.

ACCESSION BI200729 GI:14666701  
VERSION BI200729.1  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides.  
ORGANISM Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)  
AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand  
TITLE 'M. and Roe, B. Fusarium sporotrichioides EST database  
JOURNAL Unpublished (2001)  
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marlan Beremand regarding clone availability. Included  
is the best homolog from a blast search of Genbank nr 04-09-01  
633 5e-66 g1|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE  
KPECURSOR (EN  
Seq primer: T3

FEATURES  
source  
High quality sequence stop: 440.  
Location/Qualifiers

1. 450  
/organism="Fusarium sporotrichioides"  
/strain="Tri 10"  
/db\_xref="taxon:5514"  
/clone="o105f5"  
/clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed  
cDNA library"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript  
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t  
ORIGIN

Query Match 11.6%; Score 127.6; DB 13; Length 450;  
Best Local Similarity 62.0%; Pred. No. 1e-26;  
Matches 202; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

464 GTGGGCGCTCTGTGAAGCGTGTCACTACTGCTTATTTGGATTCTGTAAAGGCTCTCTGA 523  
124 GTGCTGCTTCTGGAAGTGTCACTCTGATCTGTGAGACTGTGCAAGCTTCTTGTCT 183  
524 GCTGGCCCGGTAAAGCCCAATGTCAATCTCTGTCAAGTCTGTAAAGATGTGTCA 583  
184 CTGGAGGCGCAAGCCCAAGTCAAGCCCTCTGTGCTTGTGACAAAAAGATTAACC 243  
584 CTGCCCTTAGTACAGCAATGTCCAAAGTGTGTAAAGTGTGTAAAGTGTATGTGA 643  
244 CTATCACTTAAGCTGAAGCTGTCAAGGTTGTGAAGTGTGTGTGTGTGTGTGTGT 303  
644 ACACAAACAGCGCTTGGGCTGTAAAGATATCTTGCCTATGTTGGCTGCTGCCA 703  
304 CCATCACTACTCCCTTGGGCTGTCAAGCAAGACCTTGTAGGTTTGGCTTACCAAGC 363  
704 TCAGTGTGTGTGAATCTGCTGTGCTGTTTCTTGTGAACCTTCACTTCACTTCA 763  
364 TTGCTGTGTGTGAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423  
764 CCTGTGTGTGTGAAGATGTGT 789  
Db 424 GTCCCGTAAAGGCAAGATGATT 449

RESULT 3  
BI190695 444 bp mRNA linear EST 10-JUL-2001  
LOCUS j3g10f5.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
DEFINITION library Fusarium sporotrichioides cDNA clone j3g10f5 5', mRNA  
sequence.

ACCESSION BI190695 GI:14664374  
VERSION BI190695.1  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides.  
ORGANISM Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE	Hypocretales; mitosporic Hypocretales; Fusarium.
AUTHORS	Ren,Q., Tag,A., Peplov,A., Lai,H., Kupfer,C., Peterson,A., Beremand
TITLE	1 (bases 1 to 444)
JOURNAL	'M. and Roe,B.
COMMENT	Analysis of a Fusarium sporotrichioides EST database Unpublished (2001) Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 576_36-59 g[1]170140 sp P45699 PUTATIVE ENDOGLUCANASE TYPE KPECURSOR [EN] Seq primer: T3. FEATURES Source location/Qualifiers 1..444 /organism="Fusarium sporotrichioides" /strain="Tri 10" /db_xref="taxon:5514" /clone="13g10fs" /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library" /note="Vector: pBluescript SK-; site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT	85 a     127 c     92 g     140 t
ORIGIN	
Query Match	10.8%; Score 119; DB 13; Length 444;
Best Local Similarity	62.7%; Pred.No. 3.7e-24;
Matches 185; Conservative	0; Mismatches 110; Indels 0; Gaps 0;
OY	464 GTGTGCTTCTGTGTACAGCTGTACTACTCGTTATTTGGGATTGCTGTAAAGCCTTCGTGA 523
DB	150 GTGTGCTTCTGTGTGAAGTGCCACTCTACTCATTAAGTGGAAGCTTCTTGTGCT 209
OY	524 GCTGCCCCGGATAAGGCCAATGTCAGTTTCTCGTCAATCTCTGTAAACAAGATGATGCA 583
DB	210 CTGGAGGCGCAAGCCTTAAGTCAGCGCCCTGCTCTGACTTTGTGCACAAAGAATTAAC 269
OY	584 CTGCCCTTAGTGACAGCAATGTCCAAGTGCCTGTAAAGCGTGTAAACAGTTACATGTGTA 643
DB	270 CTATCACTAACCTGAACGCTGTCAACGGTTGAGGGTGGTGGTCTTCTGCTATGCTTGCA 329
OY	644 ACGACATCACAGCTTGGGCTGTAAACGATTAATCTTGCTTAATGGTTGCTGCTGCTGCCA 703
DB	330 CCAACTACTCCCGGCGGCTGTCAACGACACCTTGTACAGGTTCCTCTACCAAGC 389
OY	704 TCAGTGGTGGTGAATCTGCGTGGTGTCTGTTGTTGGAATTAATCTTTCAC 758
DB	390 TTGCTGTGTGTAGTGAGGCAGAGCTGTGCTGTGCTATGCTCTACCTTTCAC 444
RESULT 4	
B187295	B187295 426 bp mRNA linear EST 10-JUL-2001
LOCUS	alhlifs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION	library Fusarium sporotrichioides cDNA clone alhlifs 5', mRNA
SEQUENCE	Sequence.
ACCESSION	B187295.1 GI:14660974
VERSION	EST.
KEYWORDS	Fusarium sporotrichioides.
SOURCE	Fusarium sporotrichioides
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocretales; mitosporic Hypocretales; Fusarium.
REFERENCE	1 (bases 1 to 426)
AUTHORS	Ren,Q., Tag,A., Peplov,A., Lai,H., Kupfer,C., Peterson,A., Beremand ,M. and Roe,B.

TITLE	JOURNAL	COMMENT
Analysis of a Fusarium sporotrichioides EST database	Unpublished (2001)	Other ESTs: alh11f1
Contact: Bruce A. Roe, University of Oklahoma		Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma		620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912		Fax: 405 325 7762
Email: broe@ou.edu		Contact Dr. Marian Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01		565 56-58 g[11170140]ep[P45699 PUTATIVE ENDOGLUCANASE TYPE
KREPCROR 1EN		Seq primer: T3
High quality sequence stop: 388.		Location/Qualifiers
1. .426		/organism="Fusarium sporotrichioides"
/strain="Tri 10"		/db_xref="taxon:5514"
/clone="alh11f1"		/cdna_lib="Fusarium sporotrichioides Tri 10 overexpressed
/note="vector: pBluescript SK-, Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript"		; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT	82 a	119 c 91 g 134 t
ORIGIN		
Query Match	10.3%	Score 113.2; DB 13; Length 426;
Best Local Similarity	62.2%	Pred. No. 1.9e-22;
Matches 178; Conservative	0;	Mismatches 108; Indels 0; Gaps 0;
QY	464	GTGGGCGCTGTGATGCGGTGCTACTCTGTTATGGGATTGGCTGAAGCCTCTCTGA 523
DB	140	GTGCTGCTTCGTGAAGTGGCCACTCTACTGATTACTGGAGTGTGCAAGCTTCTTCT 199
QY	524	GCTGCGCCGGTAGAGCCCAATGTCAGTTCTCTGTCAGAGTCTGTAAACAAAGATGATG 583
DB	200	CTTGAGAGCGGCAAGCTTAAGTACAGCCGCCCTGCTGACTTGATGTGACAAACAAATTAAC 259
QY	584	CTGCGCTTAGTGAACGAAATGCCAAGTGTGCTGAACGCTGTAAAGTAAAGTAACTATGCTA 643
DB	260	CTATCACTTAACCTGAACGCTGTCAACGCTGTGAGGCTGTGCTTGTATCTTGA 319
QY	644	ACGACAAACAGCCTTGGGCTGTAAAGTAACTTTCCTATGCTTTGGCTGCTGCTGCA 703
DB	320	CCAACTACTCCCGCTGGGCTGTCAACGACCACTTGTCTTACGCTTTGCTGCTCAACAGC 379
QY	704	TCAGTGTGTGTGTGAATCTGCTGCTGCTGCTTCTTGTTCGAAC 749
DB	380	TTGCTGTGTGTGTGAGGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 425
RESULT 5		
LOCUS	BI190568	215 bp mRNA linear EST 10-JUL-2001
DEFINITION	12el1f1.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA	library Fusarium sporotrichioides cDNA clone 12el1f1 5', mRNA
ACCESSION	BI190568	
VERSION	BI190568.1	GI:14664247
KEYWORDS	EST.	
SOURCE	Fusarium sporotrichioides.	
ORGANISM	Fusarium sporotrichioides	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
AUTHORS	Hypocreales; microsporid Hypocreales; Fusarium.	
	1 (bases 1 to 215)	
	Ren, Q., Tang, A., Pehl, A., Lai, H., Kupfer, C., Peterson, A., Beremand	
	M. and Roe, B.	
TITLE	Analysis of a Fusarium sporotrichioides EST database	
JOURNAL	Unpublished (2001)	

Other ESTs: 12c11fs.f1  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Contact: Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broeou.edu  
 Contact Dr. Marian Beremand regarding clone availability. Included  
 is the best homolog for a blastx search of Genbank nr 04-09-01  
 353 7e-35 g+||170140|sp|p45699 PUTATIVE ENDOGLUCINASE TYPE  
 KPECURSOR (EN

Seq primer: T3  
High quality sequence stop: 156  
Location/Qualifiers  
1. .215  
Accession="Eucarium spp

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/organism="H. influenzae"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="12cells"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript"
, 3' end of cDNA cloned into XhoI site of pBluescript"
44 a 61 C 53 g 56 t 1 others
BASE COUNT

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44 a	61 c	55 g	20 e		
------	------	------	------	--	--

Query Match	6.8%;	Score 75;	DB 13;	Length 215;
Best Local Similarity	60.6%;	Pred. No. 3e-11;		
Matches 123;	Conservative	0;	Mismatches	80;
			Indels	0;
			Gaps	0

[illegible]

Oy  
Db

556 GTCAAGTCCTGACAAAGAATGGTGTGCATCGCCCTTAGTGACACGAATAAGTCCAAAGGSC 678  
| | | | | | | | | | | | | | | | | |  
61 GCTCTGACTTGTGACACAAGAATAACCATTATCATTAACCTGAGCCTGTACACGGTTGT 120  
| | | | | | | | | | | | | | | | | |

QY  
616 TGTAAAGTGGTTACGTTACATGTGAACGCAACCATCTTGAGCCTGATACACAT...  
||||| ||||  
Db 121 GAGGTGGTGGTTCGTCTAATGCTTGACCACTACTCCCCCGTAGGCTGTCAACGACAC 180

Oy 676 CTTGCTAAGGTTGCTGCTGC 698  
||||| ||| ||||| ||||| |  
Db 181 CTTGCTAAGGTTGCTGCTAC 203

RESULT 6	LOCUS	DEFINITION
BI191461	289 bp	mRNA
BI191461		linear
		EST 10-UTL-2001
		kg10ts_r1 Fusarium sporotrichoides Tri 10 overexpressed cDNA
		kg10ts_r1 Fusarium sporotrichoides cDNA clone kg310ts 5', mRNA

Accession	Sequence
BI191461	
BI191461.1	GI:14665140
BI191461.2	
BI191461.3	
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BI191461.6	
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BI191461.8	
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BI191461.10	
BI191461.11	
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BI191461.100	

KEYWORDS  
as:  
SOURCE  
ORGANISM  
Fusarium sporotrichioides.  
Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes  
Hymenocerales; mitosporic Hymenocerales; Fusarium.

REFERENCE AUTHORS	TITLE
1 (bases 1 to 289) Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremant, M. and Roe, B.	Analysis of a Fusarium sporotrichioides EST database

unpublished (2001)  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Ov  
Tel: 405 325 4912  
Fax: 405 325 7762

Contact: broe@umich.edu  
 Email: Dr. Marien Beremand regarding clone availability. Included  
 is the best homolog from a blastx search of Genbank nr 04-09-01  
 323 6e-30 g|11170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE  
 XPRECURESOR (EN  
 Seg primer: T3  
 High quality sequence stop: 265.  
 location/Qualifiers  
 1 289  
 1..289:am="Rusarium sporocricoides"

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//strain="Tri 10"
//strain="Tacón:5514"
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/clone_id="Fusarium sporotrichoides Tri 10 overexpressed
cDNA library"
/note="Vector: p Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
' 3' end of cDNA cloned into XhoI site of pBluescript"
62 a 81 c 56 g 90 t

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500 100 200 300 400 500 600 700 800 900 1000

[illegible][illegible][illegible]

Db 253 CTATCAGCTAACCTGGAAGCTGCTGACGGTAA 205

BI187393	299 bp	mRNA	linear	EST 10-JUL-2001
LOCUS	BI187393	ab03035.r1	Fusarium sporotrichioides T11 10 overexpressed cDNA	
DEFINITION	library Fusarium sporotrichioides cDNA clone ab03035 5', mRNA sequence.			

ACCESSION B187393  
VERSION B187393.1 GI:14661072  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides.  
Fusarium sporotrichioides

ORGANISM  
Fusarium sp.; *Penicillium*; *Sordariomyces*;  
Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
Hypocreales; mitosporic Hypocreales; *Fusarium*.  
1 (bases 1 to 295)  
REFERENCE  
Pan O., Tag A., Penlow, A., Lai H., Kupfer, C., Peterson, A., Beremand

AUTHORS: 'M. and Roe, B.  
TITLE: Analysis of a Fusarium sporotrichioides EST database  
JOURNAL: Unpublished (2001)  
COMMENT: Other ESTs: a3b03fs.f1

CONTACT: Bruce A. Roe, University of Oklahoma, bioecon@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA

Tel : 405 325 4912  
Fax: 405 325 7762  
Email: broeou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
in the search of Genbank nr 04-09-01  
is the best homolog From a blastx search of ENDOGUCANASE

329 1e-30 g1|1170140|sp|P45659 FOLINATE DEHYDROGENASE  
KPRECURSOR (EN  
Seq primer: T3  
High quality sequence stop: 289.  
/0001151000

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FEATURES
  source
    Location/Qualifiers
      1. .299
        /organism="Fusarium sporotrichioides"

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Query Match 5.3%; Score 58.2; DB 13; Length 299;  
 Best Local Similarity 61.6%; Pred. No. 3.9e-06;  
 Matches 93; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

BASE COUNT 65 a 84 c 54 g 96 t

ORIGIN

Query 464 GTGTGCTCTGTGTAAGGCTGTAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 523  
 |||||  
 Db 142 GTGTGCTCTGTGTAAGGCTGTAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 201  
 |||||  
 Qy 524 GCTGCGCCGGTAAGGCCAATGTCAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 583  
 |||||  
 Db 202 CTGAGAGCGGCAAGGCTTAAGTCAAGCCGCTCTGCTCTGTAAGTCAAGCAAGATTAACC 261  
 |||||  
 Qy 584 CTGCGCTTGTAGACAGCAATGTCCAAAGTGG 614  
 |||||  
 Db 262 CTATCACTTAACCTGAACGCTGTCAACGGTTG 292  
 |||||

RESULT 8 274 bp mRNA linear EST 10-JUL-2001  
 B118678  
 LOCUS d2c10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
 DEFINITION library Fusarium sporotrichioides cDNA clone d2c10fs 5', mRNA  
 sequence.

ACCESSION B118678.1 GI:14662357  
 VERSION B118678  
 KEYWORDS Fusarium sporotrichioides.  
 SOURCE Fusarium sporotrichioides.  
 ORGANISM Fusarium sporotrichioides.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 274)  
 Ren, Q., Tag, A., Peglow, A., Lai, H., Kupfer, C., Peterson, A., Beremand  
 'M. and Roe, B.  
 TITLE Analysis of a Fusarium sporotrichioides EST database  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
 Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broe@ou.edu  
 Contact Dr. Marian Beremand regarding clone availability. Included  
 is the best homolog from a blastx search of Genbank nr 04-09-01  
 303 1e-27 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE  
 KPEPCRSOR (BN  
 Seq primer: T3  
 High quality sequence stop: 102.

FEATURES  
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 /organism="Fusarium sporotrichioides"  
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 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript  
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 62 a 80 c 49 g 83 t

ORIGIN

Query Match 5.2%; Score 57; DB 13; Length 274;  
 Best Local Similarity 62.1%; Pred. No. 8.3e-06;  
 Matches 90; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 464 GTGTGCTCTGTGTAAGGCTGTAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 523  
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 Db 127 GTGTGCTCTGTGTAAGGCTGTAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 186  
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 Qy 524 GCTGCGCCGGTAAGGCCAATGTCAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 583  
 |||||  
 Db 187 CTGAGAGCGGCAAGGCTTAAGTCAAGCCGCTCTGCTCTGTAAGTCAAGCAAGATTAACC 246  
 |||||  
 Qy 584 CTGCGCTTGTAGACAGCAATGTCCAAAGTGG 608  
 |||||  
 Db 247 CTATCACTTAACCTGAACGCTGTCAACGGTTG 271  
 |||||

RESULT 9 280 bp mRNA linear EST 10-JUL-2001  
 B1190362  
 LOCUS h4h07fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
 DEFINITION library Fusarium sporotrichioides cDNA clone h4h07fs 5', mRNA  
 sequence.

ACCESSION B1190362.1 GI:14664041  
 VERSION B1190362  
 KEYWORDS Fusarium sporotrichioides.  
 SOURCE Fusarium sporotrichioides.  
 ORGANISM Fusarium sporotrichioides.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 280)  
 Ren, Q., Tag, A., Peglow, A., Lai, H., Kupfer, C., Peterson, A., Beremand  
 'M. and Roe, B.  
 TITLE Analysis of a Fusarium sporotrichioides EST database  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
 Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broe@ou.edu  
 Contact Dr. Marian Beremand regarding clone availability. Included  
 is the best homolog from a blastx search of Genbank nr 04-09-01  
 303 1e-27 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE  
 KPEPCRSOR (BN  
 Seq primer: T3  
 High quality sequence stop: 261.

FEATURES  
 source 1..280  
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 /organism="Fusarium sporotrichioides"  
 /strain="Tri 10"  
 /db\_xref="taxon:5514"  
 /clone="h4h07fs"  
 /clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed  
 cDNA library"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript  
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 60 a 79 c 53 g 88 t

ORIGIN

Query Match 5.2%; Score 57; DB 13; Length 280;  
 Best Local Similarity 62.1%; Pred. No. 8.4e-06;  
 Matches 90; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 464 GTGTGCTCTGTGTAAGGCTGTAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 523  
 |||||  
 Db 133 GTGTGCTCTGTGTAAGGCTGTAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 192  
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 Qy 524 GCTGCGCCGGTAAGGCCAATGTCAAGTCTCTGTCAGTCCGTAACTCCGTAAACAAGATGCTGTA 583  
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Db 193 CTGGAGCGGAGAGCTAAAGTACGCGCCCTGCTGACTGTGACAAACAATTAAC 252

QY 584 CTGCCTTAGTAGACAGCATGTCCA 608

Db 253 CTATCACTAACCTGAACGCTGTCA 277

RESULT 10

LOCUS B1189728

DEFINITION B1189728 289 bp. mRNA linear EST 10-JUN-2001  
gi066f.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
library Fusarium sporotrichioides cDNA clone gi066f.5', mRNA

ACCESSION B1189728

VERSION B1189728.1

KEYWORDS GI:14663407

SOURCE EST.

ORGANISM Fusarium sporotrichioides.  
Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreales; mitosporic Hypocreales; Fusarium.  
1 (bases 1 to 289)

REFERENCE Ren, O., Tag, A., Peglow, A., Lai, H., Kupfer, C., Peterson, A., Beremand  
M., and Roe, B. Fusarium sporotrichioides EST database  
Analysis of a Fusarium sporotrichioides EST database  
Unpublished (2001)  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability included  
is the best homolog for a blastx search of Genbank nr 04-09-01  
303.1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE  
KRECKRECKOR (EN)

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

1. 289  
Location/Qualifiers  
/organism="Fusarium sporotrichioides"  
/strain="Tri 10"  
/db\_xref="taxon:5514"  
/clone="g1c06f5"  
/clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed  
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/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into XhoI site of pBluescript  
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 64 a 84 c 49 g 92 t

ORIGIN

Query Match 5.2%; Score 57; DB 13; Length 289;  
Best Local Similarity 62.1%; Pred. No. 8.6e-06;  
Matches 90; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 464 GTGTGCTCTGTGTAACGATGCTACTGCTGATTTGGATTTGCTTAAGGCTCTCTGTA 523

Db 142 GTGTGCTCTGTGTAACGATGCTACTGCTGATTTGGATTTGCTTAAGGCTCTCTGTA 201

QY 524 GTTGGCCCGTAAAGGCAATGTCAGTTCTCTGCAAGTCTGTAAACAAAGTGTGTCA 583

Db 202 CTGTGAGCGGCAAGGCTAAAGTCAAGGCGCTGCTGTGACTGTGTGCAACAAAGTAAAC 261

QY 584 CTGCCCTTAGTACACAGCAATGTCCA 608

Db 262 CTATCACTAACCTGAACGCTGTCA 286

RESULT 11

LOCUS A0013377

DEFINITION A0013377 Schizosaccharomyces pombe late log phase cDNA

ACCESSION A0013377

VERSION A0013377.1

KEYWORDS GI:3368168

SOURCE EST.

ORGANISM fission yeast.  
Schizosaccharomyces pombe  
Schizosaccharomycetes; Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetales;  
Schizosaccharomycetes.  
1 (bases 1 to 559)

REFERENCE Moriyo, M. and Mita, K.  
Identification of expressed sequence tags of Schizosaccharomyces  
pombe

AUTHORS Moriyo, M. and Mita, K.

TITLE

JOURNAL

COMMENT

Unpublished (1998)  
Contact: Mitsuo Moriyo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: moriyo@nirs.go.jp.

FEATURES

Source

1. 559  
Location/Qualifiers  
/organism="Schizosaccharomyces pombe"  
/strain="972"  
/db\_xref="taxon:4896"  
/clone="spc08072"  
/clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
/sex="n minus"  
/note="Vector: M13mp19; The cDNA library of  
Schizosaccharomyces pombe was prepared by cloning cDNA  
into the SmaI site of M13mp19 DNA and the direction of DNA  
sequences was not always from 5' to 3'. The cDNA data of  
Schizosaccharomyces pombe are available for searching on  
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 136 a 124 c 100 g 198 t

ORIGIN

Query Match 4.5%; Score 49.2; DB 9; Length 559;  
Best Local Similarity 52.7%; Pred. No. 0.0029;  
Matches 139; Conservative 0; Mismatches 113; Indels 12; Gaps 1;

QY 88 TATGTCAATGTGTGTAAGAGCTGAATGCGCCCTACTTGTGCAATCTGATCCACC 147

Db 226 TATGTCAATGTGTGTAAGAGCTGAATGCGCCCTACTTGTGCAATCTGATCCACC 285

QY 148 TGTAAAGTAAGCAAGTACTACTCTCAATGCTTGGCCCTGAAGCAAGGCAATAG 207

Db 286 TGTATCTATTAATATCCCTGGATTCGCAATGATCCAGTTG-----ATTAT 333

QY 208 TCTTCTGAATGAGAGTGTGATGTCATGATGATGATGATGATGATGATGATGATGAT 267

Db 334 ACAGAACCTGTGCMAATTAATCAACACTGCGCGGATCAATTAACATGCGCCAACT 393

QY 268 TGTTCGAATCTGATTCACCTGTAAAGTAAGCAACATTAATCTACTCTCAATGCTTGGC 327

Db 394 TGCTGTGACCGAGATCCGATGATTTTACATGTCATATTAATCTCAATGATTTCCA 453

QY 328 CTGAAGCAATGCGCAATTAACCT 351

Db 454 GTTGATATGATCCTCTTATCT 477

RESULT 12

LOCUS B0767726

DEFINITION B0767726 541 bp. mRNA linear EST 26-JUN-2002  
EBR008\_S0009\_N14\_R root, 3 week, drought-stressed, cv Optic, EBR008  
Hordeum vulgare cDNA clone EBR008\_S0009\_N14\_5', mRNA sequence.

ACCESSION B0767726

VERSION B0767726.1

KEYWORDS GI:21976200

SOURCE EST.

ORGANISM Hordeum vulgare.  
Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae



REFERENCE 1 ; Trilicaceae; Hordeum.  
AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.  
TITLE Development of Barley Transcriptome Resources  
JOURNAL Unpublished (2001)  
COMMENT Contact: Waugh R, Marshall DF  
Genome Dynamics/Computational Biology  
Scottish Crop Research Institute  
Invergowrie, Dundee, DD2 5DA, Scotland, UK  
Tel: 00 44 1382 562731  
Fax: 00 44 1382 562426  
Email: ees@scri.sari.ac.uk.

FEATURES  
source  
1. 541  
/organism="Hordeum vulgare"  
/cultivar="Optic"  
/db\_xref="taxon:4513"  
/clone="EBR08.S009.N14"  
/clone\_lib="root, 3 week, drought-stressed, cv Optic, EBR08"  
/tissue\_type="root"  
/dev\_stage="3 week"  
/lab\_host="DH10B"  
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

BASE COUNT 108 a 178 c 108 g 147 t  
ORIGIN

Query Match 4.3%; Score 46.8; DB 14; Length 541;  
Best Local Similarity 60.0%; Pred. No. 0.015;  
Matches 78; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 53 CTGAATGGCTCTGCTAAATGATAGCAAGCTATGTCATATGCTGTAGTACACT 112  
Db 235 CTGCGACGCCCTCTCCGAAACGTTGCTAGCACTACTACCAATGCGGTGCACTCACT 294  
Qy 113 GGAATGGCCTTACTGTTCGAATCTGGATCCACTGTAAGTAAGCAAGATTACTACT 172  
Db 295 GGACTGGGCCCACTCTCGCAAGACTGCTACCACTGCTTAAGCAGAACCTTACTACT 354  
Qy 173 CTCAATGTCT 182  
Db 355 ACCAGTGTGT 364

RESULT 13  
AM285303 243 bp mRNA linear EST 19-JUL-2000  
LOCUS Lgi\_237.F05.g1\_A002 Light Grown 1 (LGI) sorghum bicolor cDNA, mRNA  
DEFINITION  
ACCESSION AM285303  
VERSION AM285303.1 GI:6675147  
KEYWORDS EST.  
SOURCE sorghum.  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Sorghum.  
REFERENCE 1 (bases 1 to 243)  
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.  
TITLE An EST database from Sorghum: light-grown seedlings  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210

Email: mmpiratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: T7  
High quality sequence start: 3  
High quality sequence stop: 243  
POLYA=yes.

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1. 243  
/organism="Sorghum bicolor"  
/db\_xref="taxon:4558"  
/clone\_lib="Light Grown 1 (LGI)"  
/note="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: lambda Zap; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 51 a 66 c 53 g 73 t  
ORIGIN

Query Match 4.1%; Score 45.6; DB 10; Length 243;  
Best Local Similarity 68.5%; Pred. No. 0.019;  
Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 88 TATGTCATGCTGGTGAAGCACTGGAATGCCCTTCTGTCGAATGTGATCCACC 147  
Db 8 TACGACAGTCCGCTGTATGCTGGAATGCCCCGACCACTGCGTGGCTTACC 67  
Qy 148 TGTAAAGTAAAGCAAGATTACTTACTTCATG 179  
Db 68 TCGAAGTTTCACACCTTACTCTCGAGTG 99

RESULT 14  
AU013529 539 bp mRNA linear EST 03-AUG-1998  
LOCUS AU013529 Schizosaccharomyces pombe late log phase cDNA  
DEFINITION Schizosaccharomyces pombe cDNA clone spc08285, mRNA sequence.  
ACCESSION AU013529  
VERSION AU013529.1 GI:3368320  
KEYWORDS EST.  
SOURCE fission yeast.  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.  
REFERENCE 1 (bases 1 to 539)  
Moriyomo, M. and Mita, K.  
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mitsuoki Moriyomo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: moriyomo@nirs.go.jp.

FEATURES  
source  
1. 539  
/organism="Schizosaccharomyces pombe"  
/strain="972"  
/db\_xref="taxon:4896"  
/clone="spc08285"  
/clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
/sex="h minus"  
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 130 a 119 c 101 g 185 t 4 others  
ORIGIN

Matches	65;	CONSERVATIVE	67	INTERMEDIATE	69	PROGRESSIVE
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65	65	65	65	65		

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Oy      86  TGTATGTCATATGTCGTGTGAAGCACTGGAAATGGCCCTACTGTTGGGAATCGGATCCA 145
Db      189  TTTGGGGGCAATGCGGAGGTCAAGAGTAGAAGCGGCCGACACTAGTTGGCTTGATCTG 248

Oy      146  CCTGTAAAGTAGCAACGATTACTACTCTGCATGCTCTGC 185
Db      249  CTGTGTTCTACTTCACCCCTACTACGCTCAATGATTC 288

Search completed: June 17, 2003, 18:49:25
Job time : 1488.97 secs

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Search completed: June 17, 2003, 18:49:25  
Job time : 1488.97 secs